

# SEQUENCE LISTING

<110> Reed, John C.

<120> Novel Card Proteins Involved in Cell Death Regulation

<130> P-LJ 3650

<140> 09/388,221

<141> 1999-09-01

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<170> PatentIn Ver. 2.1

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Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg Lys Cys		
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Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His Leu Ile		1440
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Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala	
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His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr	
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Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln	
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Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe	
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Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr	
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Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
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Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
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Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu	
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Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala	
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Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro	
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Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu	
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Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg	
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Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr	
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Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu	
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Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu	
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Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val	
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Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser	
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Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly	
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Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln	
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Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile	
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Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly	
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Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu	
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Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu	
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645 650 655	
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Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala	
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His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu	
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Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu	
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Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	
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His	Ser	Arg	Ser	Ser	Ser	Gly	Glu	Thr	Pro	Ala	Gln	Pro	Glu	Lys	Thr	35	40	45	
Ser	Gly	Met	Glu	Val	Ala	Ser	Tyr	Leu	Val	Ala	Gln	Tyr	Gly	Glu	Gln	50	55	60	
Arg	Ala	Trp	Asp	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	65	70	75	80
Ser	Leu	Cys	Ala	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	85	90	95	
Pro	Tyr	Ser	Pro	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	100	105	110	
Ser	Thr	Ala	Val	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	115	120	125	
Thr	Gln	Gly	Ser	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	130	135	140	
Gly	Arg	Arg	Trp	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	145	150	155	160
Pro	Ser	Ser	Pro	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	165	170	175	
Pro	Thr	Ser	Thr	Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro	180	185	190	
Ser	Leu	Ala	Pro	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	195	200	205	
Asp	Glu	Thr	Ser	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	210	215	220	
Glu	Lys	Ser	Glu	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	225	230	235	240
Pro	Pro	Gln	Ala	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	245	250	255	

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Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val  
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Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala  
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His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu  
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Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln  
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Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val  
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Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu  
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Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val  
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Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe  
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Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val  
                     1075                      1080                      1085

Met Arg Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln  
                     1090                      1095                      1100

Phe Leu Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro  
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Leu Leu Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu  
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Pro His Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe  
                     1140                      1145                      1150

Gln Met Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala  
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Arg Val Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro  
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Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro  
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Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val  
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Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Glu  
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Leu Glu Leu Cys Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu  
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Phe Tyr Val Gly His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp  
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His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr  
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Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln	
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Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg	
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Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe	
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Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr	
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Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
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Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
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Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala	
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Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro	
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Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu	
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Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu	
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Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val	
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Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala	
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Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr	
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Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser	
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Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu	
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           1395                  1400                  1405

aag tgc aaa gat gga ctc tac caa gcc ctg aag gag acc cat cct cac 4272  
 Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His  
           1410                  1415                  1420

ctc att atg gaa ctc tgg gag aag ggc agc aaa aag gga ctc ctg cca 4320  
 Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro  
 1425                  1430                  1435                  1440

ctc agc agc tga 4332  
 Leu Ser Ser

<210> 6  
 <211> 1443  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu  
   1                  5                  10                  15  
 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala  
                   20                  25                  30  
 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr  
                   35                  40                  45  
 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln  
           50                  55                  60  
 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg  
   65                  70                  75                  80  
 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe  
                   85                  90                  95  
 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr  
                   100                  105                  110  
 Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys  
           115                  120                  125  
 Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser  
   130                  135                  140  
 Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu  
 145                  150                  155                  160  
 Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala  
                   165                  170                  175  
 Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro  
           180                  185                  190  
 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu  
           195                  200                  205

Asp	Glu	Thr	Ser	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg		
210						215					220						
Glu	Lys	Ser	Glu	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr		
225					230					235					240		
Pro	Pro	Gln	Ala	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu		
				245					250					255			
Pro	Ser	Val	Arg	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu		
			260					265					270				
Asp	Phe	Asn	Gln	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His		
	275						280					285					
Pro	Arg	Ser	Gln	Asp	Pro	Leu	Val	Lys	Arg	Ser	Trp	Pro	Asp	Tyr	Val		
	290					295					300						
Glu	Glu	Asn	Arg	Gly	His	Leu	Ile	Glu	Ile	Arg	Asp	Leu	Phe	Gly	Pro		
305					310					315					320		
Gly	Leu	Asp	Thr	Gln	Glu	Pro	Arg	Ile	Val	Ile	Leu	Gln	Gly	Ala	Ala		
				325					330					335			
Gly	Ile	Gly	Lys	Ser	Thr	Leu	Ala	Arg	Gln	Val	Lys	Glu	Ala	Trp	Gly		
			340					345					350				
Arg	Gly	Gln	Leu	Tyr	Gly	Asp	Arg	Phe	Gln	His	Val	Phe	Tyr	Phe	Ser		
		355					360					365					
Cys	Arg	Glu	Leu	Ala	Gln	Ser	Lys	Val	Val	Ser	Leu	Ala	Glu	Leu	Ile		
	370					375					380						
Gly	Lys	Asp	Gly	Thr	Ala	Thr	Pro	Ala	Pro	Ile	Arg	Gln	Ile	Leu	Ser		
385					390					395					400		
Arg	Pro	Glu	Arg	Leu	Leu	Phe	Ile	Leu	Asp	Gly	Val	Asp	Glu	Pro	Gly		
				405					410					415			
Trp	Val	Leu	Gln	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu	His	Trp	Ser	Gln		
			420					425					430				
Pro	Gln	Pro	Ala	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu	Gly	Lys	Thr	Ile		
		435						440					445				
Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln		
	450					455				460							
Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly		
465					470				475						480		
Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp		
				485					490					495			
Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu		
			500					505					510				
Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr		
		515						520				525					
Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser		
	530					535					540						
Lys	Thr	Thr	Thr	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln		
545					550					555					560		
Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala		
				565					570					575			
Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg		
			580					585					590				

Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	595	600	605
Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	610	615	620
Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	625	630	635
Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	645	650	655
Leu	Glu	Ala	Tyr	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg	660	665	670
Phe	Leu	Leu	Gly	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	675	680	685
Ile	Phe	His	Cys	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	690	695	700
Pro	Ser	Leu	Gln	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His		705	710	715
Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	725	730	735
His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	740	745	750
Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	755	760	765
Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	770	775	780
Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	785	790	795
Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	805	810	815
Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	820	825	830
Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	835	840	845
Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	850	855	860
Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	865	870	875
Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	885	890	895
Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	900	905	910
Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	915	920	925
Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	930	935	940
Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Lys	Pro	Ser	945	950	955
Val	Met	Thr	Pro	Thr	Glu	Gly	Leu	Asp	Thr	Gly	Glu	Met	Ser	Asn	Ser	965	970	975

Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser  
 980 985 990  
 His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe  
 995 1000 1005  
 Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val  
 1010 1015 1020  
 Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr  
 1025 1030 1035 1040  
 Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr Gly Pro Val  
 1045 1050 1055  
 Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe  
 1060 1065 1070  
 Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val  
 1075 1080 1085  
 Met Arg Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln  
 1090 1095 1100  
 Phe Leu Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro  
 1105 1110 1115 1120  
 Leu Leu Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu  
 1125 1130 1135  
 Pro His Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe  
 1140 1145 1150  
 Gln Met Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala  
 1155 1160 1165  
 Arg Val Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro  
 1170 1175 1180  
 Leu Gly Val Leu Leu Lys Met Ile His Asn Ala Leu Arg Phe Ile Pro  
 1185 1190 1195 1200  
 Val Thr Ser Val Val Leu Leu Tyr His Arg Val His Pro Glu Glu Val  
 1205 1210 1215  
 Thr Phe His Leu Tyr Leu Ile Pro Ser Asp Cys Ser Ile Arg Lys Ala  
 1220 1225 1230  
 Ile Asp Asp Leu Glu Met Lys Phe Gln Phe Val Arg Ile His Lys Pro  
 1235 1240 1245  
 Pro Pro Leu Thr Pro Leu Tyr Met Gly Cys Arg Tyr Thr Val Ser Gly  
 1250 1255 1260  
 Ser Gly Ser Gly Met Leu Glu Ile Leu Pro Lys Glu Leu Glu Leu Cys  
 1265 1270 1275 1280  
 Tyr Arg Ser Pro Gly Glu Asp Gln Leu Phe Ser Glu Phe Tyr Val Gly  
 1285 1290 1295  
 His Leu Gly Ser Gly Ile Arg Leu Gln Val Lys Asp Lys Lys Asp Glu  
 1300 1305 1310  
 Thr Leu Val Trp Glu Ala Leu Val Lys Pro Gly Asp Leu Met Pro Ala  
 1315 1320 1325  
 Thr Thr Leu Ile Pro Pro Ala Arg Ile Ala Val Pro Ser Pro Leu Asp  
 1330 1335 1340  
 Ala Pro Gln Leu Leu His Phe Val Asp Gln Tyr Arg Glu Gln Leu Ile  
 1345 1350 1355 1360

Ala Arg Val Thr Ser Val Glu Val Val Leu Asp Lys Leu His Gly Gln  
1365 1370 1375  
Val Leu Ser Gln Glu Gln Tyr Glu Arg Val Leu Ala Glu Asn Thr Arg  
1380 1385 1390  
Pro Ser Gln Met Arg Lys Leu Phe Ser Leu Ser Gln Ser Trp Asp Arg  
1395 1400 1405  
Lys Cys Lys Asp Gly Leu Tyr Gln Ala Leu Lys Glu Thr His Pro His  
1410 1415 1420  
Leu Ile Met Glu Leu Trp Glu Lys Gly Ser Lys Lys Gly Leu Leu Pro  
1425 1430 1435 1440  
Leu Ser Ser

<210> 7  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(1296)

<400> 7  
atg atg aga cag agg cag agc cat tat tgt tcc gtg ctg ttc ctg agt 48  
Met Met Arg Gln Arg Gln Ser His Tyr Cys Ser Val Leu Phe Leu Ser  
1 5 10 15  
gtc aac tat ctg ggg ggg aca ttc cca gga gac att tgc tca gaa gag 96  
Val Asn Tyr Leu Gly Gly Thr Phe Pro Gly Asp Ile Cys Ser Glu Glu  
20 25 30  
aat caa ata gtt tcc tct tat gct tct aaa gtc tgt ttt gag atc gaa 144  
Asn Gln Ile Val Ser Ser Tyr Ala Ser Lys Val Cys Phe Glu Ile Glu  
35 40 45  
gaa gat tat aaa aat cgt cag ttt ctg ggg cct gaa gga aat gtg gat 192  
Glu Asp Tyr Lys Asn Arg Gln Phe Leu Gly Pro Glu Gly Asn Val Asp  
50 55 60  
gtt gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc ccc 240  
Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro  
65 70 75 80  
act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg gta 288  
Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val  
85 90 95

agg gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag cac	336
Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His	
100 105 110	
ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc ccc	384
Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro	
115 120 125	
ttg ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc cac	432
Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His	
130 135 140	
ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg ttt	480
Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe	
145 150 155 160	
ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg gag cat cca gcc	528
Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala	
165 170 175	
cgg gtg gag cct ttc tat gct gtc ctg gaa agc ccc agc ttc tct ctg	576
Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu	
180 185 190	
atg ggc atc ctg ctg cgg atc gcc agt ggg act cgc ctc tcc atc ccc	624
Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro	
195 200 205	
atc act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat att	672
Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile	
210 215 220	
aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg cta aca aag gcg	720
Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala	
225 230 235 240	
ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc ctg cag act tcg	768
Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser	
245 250 255	
ccc cca atg gaa ccc ctg aac ttt ggt tcc agt tat att gtg tct aat	816
Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn	
260 265 270	
tct gct aac ctg aaa gta atg ccc aag gag ttg aaa ttg tcc tac agg	864
Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg	
275 280 285	

agc cct gga gaa att cag cac ttc tca aaa ttc tat gct ggg cag atg 912  
 Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met  
 290 295 300

aag gaa ccc att caa ctt gag att act gaa aaa aga cat ggg act ttg 960  
 Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu  
 305 310 315 320

gtg tgg gat act gag gtg aag cca gtg gat ctc cag ctt gta gct gca 1008  
 Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala  
 325 330 335

tca gcc cct cct cct ttc tca ggt gca gcc ttt gtg aag gag aac cac 1056  
 Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His  
 340 345 350

cgg caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat gat 1104  
 Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp  
 355 360 365

ctc cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg gag 1152  
 Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu  
 370 375 380

cag gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg gtg 1200  
 Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val  
 385 390 395 400

gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att agt 1248  
 Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser  
 405 410 415

gaa agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg taa 1296  
 Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu  
 420 425 430

aatgagtcag ttaggtagtc tggaagagag aatccagcgt tctcattgga aatggataaa 1356

cagaaatgtg atcattgatt tcagtgttca agacagaaga agactgggta acatctatca 1416

cacaggcttt caggacagac ttgtaacctg gcatgtacct attgactgta tcctcatgca 1476

ttttcctcaa g 1487

<210> 8  
 <211> 431  
 <212> PRT



<213> Homo sapiens

<400> 8

Met	Met	Arg	Gln	Arg	Gln	Ser	His	Tyr	Cys	Ser	Val	Leu	Phe	Leu	Ser
1				5					10					15	
Val	Asn	Tyr	Leu	Gly	Gly	Thr	Phe	Pro	Gly	Asp	Ile	Cys	Ser	Glu	Glu
			20					25					30		
Asn	Gln	Ile	Val	Ser	Ser	Tyr	Ala	Ser	Lys	Val	Cys	Phe	Glu	Ile	Glu
		35					40					45			
Glu	Asp	Tyr	Lys	Asn	Arg	Gln	Phe	Leu	Gly	Pro	Glu	Gly	Asn	Val	Asp
	50					55					60				
Val	Glu	Leu	Ile	Asp	Lys	Ser	Thr	Asn	Arg	Tyr	Ser	Val	Trp	Phe	Pro
65					70					75					80
Thr	Ala	Gly	Trp	Tyr	Leu	Trp	Ser	Ala	Thr	Gly	Leu	Gly	Phe	Leu	Val
				85					90					95	
Arg	Asp	Glu	Val	Thr	Val	Thr	Ile	Ala	Phe	Gly	Ser	Trp	Ser	Gln	His
			100					105					110		
Leu	Ala	Leu	Asp	Leu	Gln	His	His	Glu	Gln	Trp	Leu	Val	Gly	Gly	Pro
	115						120					125			
Leu	Phe	Asp	Val	Thr	Ala	Glu	Pro	Glu	Glu	Ala	Val	Ala	Glu	Ile	His
	130					135					140				
Leu	Pro	His	Phe	Ile	Ser	Leu	Gln	Gly	Glu	Val	Asp	Val	Ser	Trp	Phe
145					150					155					160
Leu	Val	Ala	His	Phe	Lys	Asn	Glu	Gly	Met	Val	Leu	Glu	His	Pro	Ala
				165				170						175	
Arg	Val	Glu	Pro	Phe	Tyr	Ala	Val	Leu	Glu	Ser	Pro	Ser	Phe	Ser	Leu
			180					185					190		
Met	Gly	Ile	Leu	Leu	Arg	Ile	Ala	Ser	Gly	Thr	Arg	Leu	Ser	Ile	Pro
	195					200						205			
Ile	Thr	Ser	Asn	Thr	Leu	Ile	Tyr	Tyr	His	Pro	His	Pro	Glu	Asp	Ile
	210				215						220				
Lys	Phe	His	Leu	Tyr	Leu	Val	Pro	Ser	Asp	Ala	Leu	Leu	Thr	Lys	Ala
225					230					235					240
Ile	Asp	Asp	Glu	Glu	Asp	Arg	Phe	His	Gly	Val	Arg	Leu	Gln	Thr	Ser
			245						250					255	
Pro	Pro	Met	Glu	Pro	Leu	Asn	Phe	Gly	Ser	Ser	Tyr	Ile	Val	Ser	Asn
			260					265					270		
Ser	Ala	Asn	Leu	Lys	Val	Met	Pro	Lys	Glu	Leu	Lys	Leu	Ser	Tyr	Arg
		275					280					285			
Ser	Pro	Gly	Glu	Ile	Gln	His	Phe	Ser	Lys	Phe	Tyr	Ala	Gly	Gln	Met
	290					295					300				
Lys	Glu	Pro	Ile	Gln	Leu	Glu	Ile	Thr	Glu	Lys	Arg	His	Gly	Thr	Leu
305					310					315					320
Val	Trp	Asp	Thr	Glu	Val	Lys	Pro	Val	Asp	Leu	Gln	Leu	Val	Ala	Ala
				325					330					335	
Ser	Ala	Pro	Pro	Pro	Phe	Ser	Gly	Ala	Ala	Phe	Val	Lys	Glu	Asn	His
			340					345					350		
Arg	Gln	Leu	Gln	Ala	Arg	Met	Gly	Asp	Leu	Lys	Gly	Val	Leu	Asp	Asp

355	360	365
Leu Gln Asp Asn Glu Val	Leu Thr Glu Asn Glu Lys	Glu Leu Val Glu
370	375	380
Gln Glu Lys Thr Arg Gln Ser	Lys Asn Glu Ala Leu Leu	Ser Met Val
385	390	395
Glu Lys Lys Gly Asp Leu Ala	Leu Asp Val Leu Phe Arg	Ser Ile Ser
405	410	415
Glu Arg Asp Pro Tyr Leu Val	Ser Tyr Leu Arg Gln Gln	Asn Leu
420	425	430

<210> 9

<211> 4556

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(4362)

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 9

atg gct ggc gga gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg	48
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu	
1 5 10 15	
aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg	96
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala	
20 25 30	
cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg	144
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr	
35 40 45	
agt ggc atg gag gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag	192
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln	
50 55 60	
cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg	240
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg	
65 70 75 80	
tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc	288
Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe	

85										90					95					
ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc	336																			
Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr																				
100 105 110																				
tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc	384																			
Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys																				
115 120 125																				
acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct	432																			
Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser																				
130 135 140																				
gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt	480																			
Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu																				
145 150 155 160																				
cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc	528																			
Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala																				
165 170 175																				
ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc	576																			
Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro																				
180 185 190																				
agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg	624																			
Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu																				
195 200 205																				
gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga	672																			
Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg																				
210 215 220																				
gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg	720																			
Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr																				
225 230 235 240																				
ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag	768																			
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu																				
245 250 255																				
cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag	816																			
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu																				
260 265 270																				
gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac	864																			
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His																				

275	280	285	
ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg			912
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val			
290	295	300	
gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca			960
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro			
305	310	315	320
ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct			1008
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala			
	325	330	335
gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg			1056
Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly			
	340	345	350
aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc			1104
Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser			
	355	360	365
tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc			1152
Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile			
370	375	380	
gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct			1200
Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser			
385	390	395	400
agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga			1248
Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly			
	405	410	415
tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag			1296
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln			
	420	425	430
cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata			1344
Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile			
	435	440	445
ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag			1392
Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln			
450	455	460	
aac ctc att cct tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg			1440
Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly			

465	470	475	480	
ttc tct gag tcc agc agg aag gaa tat	ttc tac aga tat ttc aca gat	1488		
Phe Ser Glu Ser Ser Arg Lys Glu Tyr	Phe Tyr Arg Tyr Phe Thr Asp			
485	490		495	
gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag	1536			
Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu				
500	505		510	
ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act	1584			
Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr				
515	520		525	
tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc	1632			
Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser				
530	535		540	
aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa	1680			
Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln				
545	550		555	560
gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct	1728			
Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala				
565	570		575	
gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg	1776			
Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg				
580	585		590	
aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt	1824			
Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly				
595	600		605	
att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc	1872			
Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu				
610	615		620	
tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag	1920			
Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu				
625	630		635	640
aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg	1968			
Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr				
645	650		655	
cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt	2016			
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg				

660	665	670	
ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac			2064
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn			
675	680	685	
atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc			2112
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val			
690	695	700	
ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac			2160
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His			
705	710	715	720
tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc			2208
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala			
725	730	735	
cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta			2256
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu			
740	745	750	
gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag			2304
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln			
755	760	765	
ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta			2352
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val			
770	775	780	
gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc			2400
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu			
785	790	795	800
ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt			2448
Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser			
805	810	815	
gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg			2496
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu			
820	825	830	
aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc			2544
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly			
835	840	845	
ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac			2592
Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn			

850	855	860	
cag acc ctg acc gag ctg gac ctg agc ttc aat gtg ctc acg gat gct			2640
Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala			
865	870	875	880
gga gcc aaa cac ctt tgc cag aga ctg aga cag ccg agc tgc aag cta			2688
Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu			
	885	890	895
cag cga ctg cag ctg gtc agc tgt ggc ctc acg tct gac tgc tgc cag			2736
Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln			
	900	905	910
gac ctg gcc tct gtg ctt agt gcc agc ccc agc ctg aag gag cta gac			2784
Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp			
	915	920	925
ctg cag cag aac aac ctg gat gac gtt ggc gtg cga ctg ctc tgt gag			2832
Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu			
	930	935	940
ggg ctc agg cat cct gcc tgc aaa ctc ata cgc ctg ggg ctg gac cag			2880
Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln			
945	950	955	960
aca act ctg agt gat gag atg agg cag gaa ctg agg gcc ctg gag cag			2928
Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln			
	965	970	975
gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg			2976
Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met			
	980	985	990
acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc			3024
Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser			
	995	1000	1005
tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt			3072
Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val			
1010	1015	1020	
gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att			3120
Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile			
1025	1030	1035	1040
gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc			3168
Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu			

1045	1050	1055	
ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg aag cct			3216
Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro			
1060	1065	1070	
ttg ggg act gac gat gac ttt ctg ggg cct gaa gga aat gtg gat gtt			3264
Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val Asp Val			
1075	1080	1085	
gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc ccc act			3312
Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe Pro Thr			
1090	1095	1100	
gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg gta agg			3360
Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu Val Arg			
1105	1110	1115	1120
gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag cac ctg			3408
Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln His Leu			
1125	1130	1135	
gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc ccc ttg			3456
Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly Pro Leu			
1140	1145	1150	
ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc cac ctc			3504
Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile His Leu			
1155	1160	1165	
ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg ttt ctc			3552
Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe Leu			
1170	1175	1180	
gtt gcc cat ttt aag aat gaa ggg atg gtc ctg gag cat cca gcc cgg			3600
Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala Arg			
1185	1190	1195	1200
gtg gag cct ttc tat gct gtc ctg gaa agc ccc agc ttc tct ctg atg			3648
Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu Met			
1205	1210	1215	
ggc atc ctg ctg cgg atc gcc agt ggg act cgc ctc tcc atc ccc atc			3696
Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro Ile			
1220	1225	1230	
act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat att aag			3744
Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile Lys			



1235	1240	1245	
ttc cac ttg tac ctt gtc ccc agc gac gcc ttg cta aca aag gcg ata			3792
Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala Ile			
1250	1255	1260	
gat gat gag gaa gat cgc ttc cat ggt gtg cgc ctg cag act tcg ccc			3840
Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser Pro			
1265	1270	1275	1280
cca atg gaa ccc ctg aac ttt ggt tcc agt tat att gtg tct aat tct			3888
Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn Ser			
	1285	1290	1295
gct aac ctg aaa gta atg ccc aag gag ttg aaa ttg tcc tac agg agc			3936
Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg Ser			
	1300	1305	1310
cct gga gaa att cag cac ttc tca aaa ttc tat gct ggg cag atg aag			3984
Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met Lys			
	1315	1320	1325
gaa ccc att caa ctt gag att act gaa aaa aga cat ggg act ttg gtg			4032
Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu Val			
1330	1335	1340	
tgg gat act gag gtg aag cca gtg gat ctc cag ctt gta gct gca tca			4080
Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala Ser			
1345	1350	1355	1360
gcc cct cct cct ttc tca ggt gca gcc ttt gtg aag gag aac cac cgg			4128
Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His Arg			
	1365	1370	1375
caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat gat ctc			4176
Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp Leu			
	1380	1385	1390
cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg gag cag			4224
Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu Gln			
1395	1400	1405	
gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg gtg gag			4272
Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val Glu			
1410	1415	1420	
aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att agt gaa			4320
Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser Glu			

1425	1430	1435	1440	
agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg				4362
Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu				
	1445	1450		
taaaatgagt cagttaggta gtctggaaga gagaatccag cgttctcatt ggaaatggat				4422
aaacagaaat gtgatcattg atttcagtgt tcaagacaga agaagactgg gtaacatcta				4482
tcacacaggc tttcaggaca gacttgtaac ctggcatgta cctattgact gtatcctcat				4542
gcattttcct caag				4556

<210> 10  
 <211> 1454  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: Synthetic Construct

<400> 10  
 Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu  
 1 5 10 15  
 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala  
 20 25 30  
 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr  
 35 40 45  
 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln  
 50 55 60  
 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg  
 65 70 75 80  
 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe  
 85 90 95  
 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr  
 100 105 110  
 Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys  
 115 120 125  
 Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser

130	135	140														
Gly	Arg	Arg	Trp	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	
145					150					155					160	
Pro	Ser	Ser	Pro	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	
				165					170					175		
Pro	Thr	Ser	Thr	Ala	Val	Leu	Gly	Ser	Trp	Gly	Ser	Pro	Pro	Gln	Pro	
			180					185						190		
Ser	Leu	Ala	Pro	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	
	195						200					205				
Asp	Glu	Thr	Ser	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	
210						215					220					
Glu	Lys	Ser	Glu	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	
225					230					235				240		
Pro	Pro	Gln	Ala	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	
				245					250					255		
Pro	Ser	Val	Arg	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu	
			260					265					270			
Asp	Phe	Asn	Gln	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His	
	275						280					285				
Pro	Arg	Ser	Gln	Asp	Pro	Leu	Val	Lys	Arg	Ser	Trp	Pro	Asp	Tyr	Val	
290						295					300					
Glu	Glu	Asn	Arg	Gly	His	Leu	Ile	Glu	Ile	Arg	Asp	Leu	Phe	Gly	Pro	
305					310					315				320		
Gly	Leu	Asp	Thr	Gln	Glu	Pro	Arg	Ile	Val	Ile	Leu	Gln	Gly	Ala	Ala	
				325					330					335		
Gly	Ile	Gly	Lys	Ser	Thr	Leu	Ala	Arg	Gln	Val	Lys	Glu	Ala	Trp	Gly	
			340					345					350			
Arg	Gly	Gln	Leu	Tyr	Gly	Asp	Arg	Phe	Gln	His	Val	Phe	Tyr	Phe	Ser	
			355				360					365				
Cys	Arg	Glu	Leu	Ala	Gln	Ser	Lys	Val	Val	Ser	Leu	Ala	Glu	Leu	Ile	
370						375					380					
Gly	Lys	Asp	Gly	Thr	Ala	Thr	Pro	Ala	Pro	Ile	Arg	Gln	Ile	Leu	Ser	

385		390		395		400									
Arg	Pro	Glu	Arg	Leu	Leu	Phe	Ile	Leu	Asp	Gly	Val	Asp	Glu	Pro	Gly
				405					410					415	
Trp	Val	Leu	Gln	Glu	Pro	Ser	Ser	Glu	Leu	Cys	Leu	His	Trp	Ser	Gln
			420					425					430		
Pro	Gln	Pro	Ala	Asp	Ala	Leu	Leu	Gly	Ser	Leu	Leu	Gly	Lys	Thr	Ile
		435					440					445			
Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln
		450				455					460				
Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly
465					470					475				480	
Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp
				485					490					495	
Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu
			500					505					510		
Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr
		515					520					525			
Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser
		530				535					540				
Lys	Thr	Thr	Thr	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln
545					550					555				560	
Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala
				565					570					575	
Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg
			580					585					590		
Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly
		595					600					605			
Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu
		610				615					620				
Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu
625					630					635				640	
Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr

	645		650		655	
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg						
	660		665		670	
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn						
	675		680		685	
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val						
	690		695		700	
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His						
705		710		715		720
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala						
	725		730		735	
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu						
	740		745		750	
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln						
	755		760		765	
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val						
	770		775		780	
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu						
785		790		795		800
Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser						
	805		810		815	
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu						
	820		825		830	
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly						
	835		840		845	
Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn						
	850		855		860	
Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala						
865		870		875		880
Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu						
	885		890		895	
Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln						

900					905					910						
Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	
915					920					925						
Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	
930					935					940						
Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	
945					950					955					960	
Thr	Thr	Leu	Ser	Asp	Glu	Met	Arg	Gln	Glu	Leu	Arg	Ala	Leu	Glu	Gln	
965					970					975						
Glu	Lys	Pro	Gln	Leu	Leu	Ile	Phe	Ser	Arg	Arg	Lys	Pro	Ser	Val	Met	
980					985					990						
Thr	Pro	Thr	Glu	Gly	Leu	Asp	Thr	Gly	Glu	Met	Ser	Asn	Ser	Thr	Ser	
995					1000					1005						
Ser	Leu	Lys	Arg	Gln	Arg	Leu	Gly	Ser	Glu	Arg	Ala	Ala	Ser	His	Val	
1010					1015					1020						
Ala	Gln	Ala	Asn	Leu	Lys	Leu	Leu	Asp	Val	Ser	Lys	Ile	Phe	Pro	Ile	
1025					1030					1035					1040	
Ala	Glu	Ile	Ala	Glu	Glu	Ser	Ser	Pro	Glu	Val	Val	Pro	Val	Glu	Leu	
1045					1050					1055						
Leu	Cys	Val	Pro	Ser	Pro	Ala	Ser	Gln	Gly	Asp	Leu	His	Thr	Lys	Pro	
1060					1065					1070						
Leu	Gly	Thr	Asp	Asp	Asp	Phe	Leu	Gly	Pro	Glu	Gly	Asn	Val	Asp	Val	
1075					1080					1085						
Glu	Leu	Ile	Asp	Lys	Ser	Thr	Asn	Arg	Tyr	Ser	Val	Trp	Phe	Pro	Thr	
1090					1095					1100						
Ala	Gly	Trp	Tyr	Leu	Trp	Ser	Ala	Thr	Gly	Leu	Gly	Phe	Leu	Val	Arg	
1105					1110					1115					1120	
Asp	Glu	Val	Thr	Val	Thr	Ile	Ala	Phe	Gly	Ser	Trp	Ser	Gln	His	Leu	
1125					1130					1135						
Ala	Leu	Asp	Leu	Gln	His	His	Glu	Gln	Trp	Leu	Val	Gly	Gly	Pro	Leu	
1140					1145					1150						
Phe	Asp	Val	Thr	Ala	Glu	Pro	Glu	Glu	Ala	Val	Ala	Glu	Ile	His	Leu	

1155	1160	1165
Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp Phe Leu		
1170	1175	1180
Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro Ala Arg		
1185	1190	1195 1200
Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser Leu Met		
1205	1210	1215
Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile Pro Ile		
1220	1225	1230
Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp Ile Lys		
1235	1240	1245
Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys Ala Ile		
1250	1255	1260
Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr Ser Pro		
1265	1270	1275 1280
Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser Asn Ser		
1285	1290	1295
Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr Arg Ser		
1300	1305	1310
Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln Met Lys		
1315	1320	1325
Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr Leu Val		
1330	1335	1340
Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala Ala Ser		
1345	1350	1355 1360
Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn His Arg		
1365	1370	1375
Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp Asp Leu		
1380	1385	1390
Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val Glu Gln		
1395	1400	1405
Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met Val Glu		

1410	1415	1420	
Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile Ser Glu			
1425	1430	1435	1440
Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu			
1445	1450		
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<213> Artificial Sequence			
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<222> (1)..(4272)			
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<223> Description of Artificial Sequence: Synthetic Construct			
<400> 11			
atg gct ggc gga gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg			48
Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu			
1 5 10 15			
aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg			96
Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala			
20 25 30			
cac tcc agg agc tct tcg ggt gag aca ccc gct cag cca gag aag acg			144
His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr			
35 40 45			
agt ggc atg gag gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag			192
Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln			
50 55 60			
cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg			240
Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg			
65 70 75 80			
tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc			288
Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe			
85 90 95			



ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc	336
Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr	
100 105 110	
tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc	384
Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys	
115 120 125	
acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct	432
Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser	
130 135 140	
gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt	480
Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu	
145 150 155 160	
cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc	528
Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala	
165 170 175	
ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc	576
Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro	
180 185 190	
agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg	624
Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu	
195 200 205	
gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga	672
Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg	
210 215 220	
gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg	720
Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr	
225 230 235 240	
ccc cca cag gcg cac acc agc cta cag ccc cac cac cac cca tgg gag	768
Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu	
245 250 255	
cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag	816
Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu	
260 265 270	
gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac	864
Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His	
275 280 285	

ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg	912
Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val	
290 295 300	
 gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca	960
Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro	
305 310 315 320	
 ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct	1008
Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala	
325 330 335	
 gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg	1056
Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly	
340 345 350	
 aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc	1104
Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser	
355 360 365	
 tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc	1152
Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile	
370 375 380	
 gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct	1200
Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser	
385 390 395 400	
 agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga	1248
Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly	
405 410 415	
 tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag	1296
Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln	
420 425 430	
 cca cag ccg gcg gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata	1344
Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile	
435 440 445	
 ctt ccc gag gca tcc ttc ctg atc acg gct cgg acc aca gct ctg cag	1392
Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln	
450 455 460	
 aac ctc att cct tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg	1440
Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly	
465 470 475 480	

ttc tct gag tcc agc agg aag gaa tat ttc tac aga tat ttc aca gat	1488
Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp	
485 490 495	
gaa agg caa gca att aga gcc ttt agg ttg gtc aaa tca aac aaa gag	1536
Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu	
500 505 510	
ctc tgg gcc ctg tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act	1584
Leu Trp Ala Leu Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr	
515 520 525	
tgc ctg atg cag cag atg aag cgg aag gaa aaa ctc aca ctg act tcc	1632
Cys Leu Met Gln Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser	
530 535 540	
aag acc acc aca acc ctc tgt cta cat tac ctt gcc cag gct ctc caa	1680
Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln	
545 550 555 560	
gct cag cca ttg gga ccc cag ctc aga gac ctc tgc tct ctg gct gct	1728
Ala Gln Pro Leu Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala	
565 570 575	
gag ggc atc tgg caa aaa aag acc ctt ttc agt cca gat gac ctc agg	1776
Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg	
580 585 590	
aag cat ggg tta gat ggg gcc atc atc tcc acc ttc ttg aag atg ggt	1824
Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly	
595 600 605	
att ctt caa gag cac ccc atc cct ctg agc tac agc ttc att cac ctc	1872
Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu	
610 615 620	
tgt ttc caa gag ttc ttt gca gca atg tcc tat gtc ttg gag gat gag	1920
Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu	
625 630 635 640	
aag ggg aga ggt aaa cat tct aat tgc atc ata gat ttg gaa aag acg	1968
Lys Gly Arg Gly Lys His Ser Asn Cys Ile Ile Asp Leu Glu Lys Thr	
645 650 655	
cta gaa gca tat gga ata cat ggc ctg ttt ggg gca tca acc aca cgt	2016
Leu Glu Ala Tyr Gly Ile His Gly Leu Phe Gly Ala Ser Thr Thr Arg	
660 665 670	

ttc cta ttg ggc ctg tta agt gat gag ggg gag aga gag atg gag aac	2064
Phe Leu Leu Gly Leu Leu Ser Asp Glu Gly Glu Arg Glu Met Glu Asn	
675 680 685	
atc ttt cac tgc cgg ctg tct cag ggg agg aac ctg atg cag tgg gtc	2112
Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val	
690 695 700	
ccg tcc ctg cag ctg ctg ctg cag cca cac tct ctg gag tcc ctc cac	2160
Pro Ser Leu Gln Leu Leu Leu Gln Pro His Ser Leu Glu Ser Leu His	
705 710 715 720	
tgc ttg tac gag act cgg aac aaa acg ttc ctg aca caa gtg atg gcc	2208
Cys Leu Tyr Glu Thr Arg Asn Lys Thr Phe Leu Thr Gln Val Met Ala	
725 730 735	
cat ttc gaa gaa atg ggc atg tgt gta gaa aca gac atg gag ctc tta	2256
His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu	
740 745 750	
gtg tgc act ttc tgc att aaa ttc agc cgc cac gtg aag aag ctt cag	2304
Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln	
755 760 765	
ctg att gag ggc agg cag cac aga tca aca tgg agc ccc acc atg gta	2352
Leu Ile Glu Gly Arg Gln His Arg Ser Thr Trp Ser Pro Thr Met Val	
770 775 780	
gtc ctg ttc agg tgg gtc cca gtc aca gat gcc tat tgg cag att ctc	2400
Val Leu Phe Arg Trp Val Pro Val Thr Asp Ala Tyr Trp Gln Ile Leu	
785 790 795 800	
ttc tcc gtc ctc aag gtc acc aga aac ctg aag gag ctg gac cta agt	2448
Phe Ser Val Leu Lys Val Thr Arg Asn Leu Lys Glu Leu Asp Leu Ser	
805 810 815	
gga aac tcg ctg agc cac tct gca gtg aag agt ctt tgt aag acc ctg	2496
Gly Asn Ser Leu Ser His Ser Ala Val Lys Ser Leu Cys Lys Thr Leu	
820 825 830	
aga cgc cct cgc tgc ctc ctg gag acc ctg cgg ttg gct ggc tgt ggc	2544
Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly	
835 840 845	
ctc aca gct gag gac tgc aag gac ctt gcc ttt ggg ctg aga gcc aac	2592
Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn	
850 855 860	



gat gtt gag ttg att gat aag agc aca aac aga tac agc gtt tgg ttc	3216
Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe	
1060 1065 1070	
ccc act gct ggc tgg tat ctg tgg tca gcc aca ggc ctc ggc ttc ctg	3264
Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu	
1075 1080 1085	
gta agg gat gag gtc aca gtg acg att gcg ttt ggt tcc tgg agt cag	3312
Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln	
1090 1095 1100	
cac ctg gcc ctg gac ctg cag cac cat gaa cag tgg ctg gtg ggc ggc	3360
His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly	
1105 1110 1115 1120	
ccc ttg ttt gat gtc act gca gag cca gag gag gct gtc gcc gaa atc	3408
Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile	
1125 1130 1135	
cac ctc ccc cac ttc atc tcc ctc caa ggt gag gtg gac gtc tcc tgg	3456
His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp	
1140 1145 1150	
ttt ctc gtt gcc cat ttt aag aat gaa ggg atg gtc ctg gag cat cca	3504
Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro	
1155 1160 1165	
gcc cgg gtg gag cct ttc tat gct gtc ctg gaa agc ccc agc ttc tct	3552
Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser	
1170 1175 1180	
ctg atg ggc atc ctg ctg cgg atc gcc agt ggg act cgc ctc tcc atc	3600
Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile	
1185 1190 1195 1200	
ccc atc act tcc aac aca ttg atc tat tat cac ccc cac ccc gaa gat	3648
Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp	
1205 1210 1215	
att aag ttc cac ttg tac ctt gtc ccc agc gac gcc ttg cta aca aag	3696
Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys	
1220 1225 1230	
gcg ata gat gat gag gaa gat cgc ttc cat ggt gtg cgc ctg cag act	3744
Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr	
1235 1240 1245	

tcg ccc cca atg gaa ccc ctg aac ttt ggt tcc agt tat att gtg tct	3792
Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser	
1250 1255 1260	
aat tct gct aac ctg aaa gta atg ccc aag gag ttg aaa ttg tcc tac	3840
Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr	
1265 1270 1275 1280	
agg agc cct gga gaa att cag cac ttc tca aaa ttc tat gct ggg cag	3888
Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln	
1285 1290 1295	
atg aag gaa ccc att caa ctt gag att act gaa aaa aga cat ggg act	3936
Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr	
1300 1305 1310	
ttg gtg tgg gat act gag gtg aag cca gtg gat ctc cag ctt gta gct	3984
Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala	
1315 1320 1325	
gca tca gcc cct cct cct ttc tca ggt gca gcc ttt gtg aag gag aac	4032
Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn	
1330 1335 1340	
cac cgg caa ctc caa gcc agg atg ggg gac ctg aaa ggg gtg ctc gat	4080
His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp	
1345 1350 1355 1360	
gat ctc cag gac aat gag gtt ctt act gag aat gag aag gag ctg gtg	4128
Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val	
1365 1370 1375	
gag cag gaa aag aca cgg cag agc aag aat gag gcc ttg ctg agc atg	4176
Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met	
1380 1385 1390	
gtg gag aag aaa ggg gac ctg gcc ctg gac gtg ctc ttc aga agc att	4224
Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile	
1395 1400 1405	
agt gaa agg gac cct tac ctc gtg tcc tat ctt aga cag cag aat ttg	4272
Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu	
1410 1415 1420	
taaaatgagt cagttaggta gtctggaaga gagaatccag cgttctcatt ggaaatggat	4332
aaacagaaat gtgatcattg atttcagtgt tcaagacaga agaagactgg gtaacatcta	4392

tcacacaggc ttccaggaca gacttgtaac ctggcatgta cctattgact gtatcctcat 4452  
gcattttcct caag 4466

<210> 12  
<211> 1424  
<212> PRT  
<213> Artificial Sequence  
<223> Description of Artificial Sequence: Synthetic Construct

<400> 12

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu  
1 5 10 15

Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala  
20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr  
35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln  
50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg  
65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe  
85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr  
100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys  
115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser  
130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu  
145 150 155 160

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala  
165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro  
180 185 190



Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu  
 195 200 205

Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg  
 210 215 220

Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr  
 225 230 235 240

Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu  
 245 250 255

Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu  
 260 265 270

Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His  
 275 280 285

Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val  
 290 295 300

Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro  
 305 310 315 320

Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala  
 325 330 335

Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly  
 340 345 350

Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser  
 355 360 365

Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile  
 370 375 380

Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser  
 385 390 395 400

Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly  
 405 410 415

Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln  
 420 425 430

Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile  
 435 440 445

Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln	450	455	460	
Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly	465	470	475	480
Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp	485	490	495	
Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu	500	505	510	
Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr	515	520	525	
Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser	530	535	540	
Lys	Thr	Thr	Thr	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln	545	550	555	560
Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala	565	570	575	
Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg	580	585	590	
Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly	595	600	605	
Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	610	615	620	
Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	625	630	635	640
Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	645	650	655	
Leu	Glu	Ala	Tyr	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg	660	665	670	
Phe	Leu	Leu	Gly	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	675	680	685	
Ile	Phe	His	Cys	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	690	695	700	

Pro	Ser	Leu	Gln	Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His
705						710				715					720
Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala
				725					730					735	
His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu
			740					745					750		
Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln
		755					760					765			
Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val
		770				775					780				
Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu
785					790					795					800
Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser
				805					810					815	
Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu
			820					825					830		
Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly
		835					840					845			
Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn
		850				855					860				
Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala
865					870					875					880
Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu
				885					890					895	
Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln
			900					905					910		
Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp
		915					920					925			
Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu
					930		935				940				
Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Lys	Pro	Ser
945					950					955					960

Val Met Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser			
	965	970	975
Thr Ser Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser			
	980	985	990
His Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe			
	995	1000	1005
Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val			
	1010	1015	1020
Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr			
	1025	1030	1035
			1040
Lys Pro Leu Gly Thr Asp Asp Asp Phe Leu Gly Pro Glu Gly Asn Val			
	1045	1050	1055
Asp Val Glu Leu Ile Asp Lys Ser Thr Asn Arg Tyr Ser Val Trp Phe			
	1060	1065	1070
Pro Thr Ala Gly Trp Tyr Leu Trp Ser Ala Thr Gly Leu Gly Phe Leu			
	1075	1080	1085
Val Arg Asp Glu Val Thr Val Thr Ile Ala Phe Gly Ser Trp Ser Gln			
	1090	1095	1100
His Leu Ala Leu Asp Leu Gln His His Glu Gln Trp Leu Val Gly Gly			
	1105	1110	1115
			1120
Pro Leu Phe Asp Val Thr Ala Glu Pro Glu Glu Ala Val Ala Glu Ile			
	1125	1130	1135
His Leu Pro His Phe Ile Ser Leu Gln Gly Glu Val Asp Val Ser Trp			
	1140	1145	1150
Phe Leu Val Ala His Phe Lys Asn Glu Gly Met Val Leu Glu His Pro			
	1155	1160	1165
Ala Arg Val Glu Pro Phe Tyr Ala Val Leu Glu Ser Pro Ser Phe Ser			
	1170	1175	1180
Leu Met Gly Ile Leu Leu Arg Ile Ala Ser Gly Thr Arg Leu Ser Ile			
	1185	1190	1195
			1200
Pro Ile Thr Ser Asn Thr Leu Ile Tyr Tyr His Pro His Pro Glu Asp			
	1205	1210	1215

Ile Lys Phe His Leu Tyr Leu Val Pro Ser Asp Ala Leu Leu Thr Lys  
1220 1225 1230

Ala Ile Asp Asp Glu Glu Asp Arg Phe His Gly Val Arg Leu Gln Thr  
1235 1240 1245

Ser Pro Pro Met Glu Pro Leu Asn Phe Gly Ser Ser Tyr Ile Val Ser  
1250 1255 1260

Asn Ser Ala Asn Leu Lys Val Met Pro Lys Glu Leu Lys Leu Ser Tyr  
1265 1270 1275 1280

Arg Ser Pro Gly Glu Ile Gln His Phe Ser Lys Phe Tyr Ala Gly Gln  
1285 1290 1295

Met Lys Glu Pro Ile Gln Leu Glu Ile Thr Glu Lys Arg His Gly Thr  
1300 1305 1310

Leu Val Trp Asp Thr Glu Val Lys Pro Val Asp Leu Gln Leu Val Ala  
1315 1320 1325

Ala Ser Ala Pro Pro Pro Phe Ser Gly Ala Ala Phe Val Lys Glu Asn  
1330 1335 1340

His Arg Gln Leu Gln Ala Arg Met Gly Asp Leu Lys Gly Val Leu Asp  
1345 1350 1355 1360

Asp Leu Gln Asp Asn Glu Val Leu Thr Glu Asn Glu Lys Glu Leu Val  
1365 1370 1375

Glu Gln Glu Lys Thr Arg Gln Ser Lys Asn Glu Ala Leu Leu Ser Met  
1380 1385 1390

Val Glu Lys Lys Gly Asp Leu Ala Leu Asp Val Leu Phe Arg Ser Ile  
1395 1400 1405

Ser Glu Arg Asp Pro Tyr Leu Val Ser Tyr Leu Arg Gln Gln Asn Leu  
1410 1415 1420

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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32

<210> 14

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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31

<210> 16

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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30

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<211> 21

<212> DNA

<213> Homo sapiens

<400> 17

tgtgatgaga gaagcgggtga c

21

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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30